

SEQUENCE LISTING

<110> Guillemette, Chantal

<120> Method for determining predisposition to
a physiological reaction in a patient

<130> 6013-118US

<150> PCT/2003/001269

<151> 2003-08-20

<150> 60/412,002

<151> 2002-09-20

<160> 71

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<213> Homo sapiens

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cgctggacgg caccattg 18

<210> 8

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<223> UGT1A7 #17 (Reverse)

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22

<210> 9
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<223> UGT1A7 #122 (Forward)

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<210> 10
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<223> UGT1A7 #123 (Reverse)

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19

<210> 11
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<223> UGT1A9 #7 (Forward)

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<210> 12
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<212> DNA

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<210> 18

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<212> DNA

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<223> ASO UGT1A7 G115 (Forward)

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<210> 19

<211> 17

<212> DNA

<213> Homo sapiens

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<223> ASO UGT1A7 S115 (Forward)

<400> 19

catccaatag tatttttt

17

<210> 20

<211> 19

<212> DNA

<213> Homo sapiens

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<222> (1)...(19)

<223> Taqman UGT1A7 codon 139/131 #387 (Forward)

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19

<210> 21

<211> 22

<212> DNA

<213> Homo sapiens

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<222> (1)...(22)

<223> Taqman UGT1A7 codon 139/131 #388 (Reverse)

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<210> 22

<211> 16

<212> DNA

<213> Homo sapiens

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<222> (1)...(16)

<223> Taqman UGT1A7 codon 139/131 K129/K131-FAM
(Forward)

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16

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<212> DNA

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<222> (1)...(17)

<223> Taqman UGT1A7 codon 139/131 K129/K131-TET
(Forward)

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<210> 24

<211> 26

<212> DNA

<213> Homo sapiens

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<222> (1)...(26)

<223> Taqman UGT1A7 codon 139 #546 (Forward)

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26

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<212> DNA

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<210> 27
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 <223> Taqman UGT1A7 codon 139 D139-Vic (Forward)

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<400> 29

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31

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<212> DNA

<213> Homo sapiens

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<222> (1)...(34)

<223> Forward M33T UGT1A9

<400> 30

gctactggta gtgcccacgg atgggagcca ctgg

34

<210> 31

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<212> DNA

<213> Homo sapiens

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<222> (1)...(34)

<223> Reverse M33T UGT1A9

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34

<210> 32

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<212> DNA

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<222> (1)...(45)

<223> Forward E139D UGT1A7

<400> 32

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45

<210> 33

<211> 45

<212> DNA

<213> Homo sapiens

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<222> (1)...(45)

<223> Reverse E139D UGT1A7

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<210> 34

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<212> DNA

<213> Homo sapiens

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<222> (1)...(23)

<223> Forward G115S UGT1A7

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23

<210> 35

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<212> DNA

<213> Homo sapiens

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<222> (1)...(23)

<223> Reverse G115S UGT1A7

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23

<210> 36

<211> 2585

<212> DNA

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<220>

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<222> (1)...(2585)

<223> UGT1A9*1

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<212> DNA

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<223> UGT1A9*2

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atacc						2585

<210> 38

<211> 2585

<212> DNA

<213> Homo sapiens

<220>

<221> allele

<222> (1)... (2585)

<223> UGT1A9*3

<400> 38

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<213> Homo sapiens

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<223> UGT1A9 Haplotype 1

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<213> Homo sapiens

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<223> UGT1A9 Haplotype 2

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<212> DNA

<213> Homo sapiens

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<223> UGT1A9 Haplotype 3

<400> 41

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<212> DNA

<213> Homo sapiens

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<221> allele

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<223> UGT1A9 Haplotype 4

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 <223> UHT1A9 Haplotype 5

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<400> 48

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<213> Homo sapiens

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<223> UGT1A9 Haplotype 11

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<213> Homo sapiens

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<223> UGT1A9 Haplotype 12

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<213> Homo sapiens

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<223> UGT1A9 Haplotype 15

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2372

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<210> 59

<211> 2372

<212> DNA

<213> Homo sapiens

<220>

<221> allele

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<223> UGT1A9 Haplotype 21

<400> 59

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<210> 60

<211> 1229

<212> DNA

<213> Homo sapiens

<220>

<221> allele

<222> (1) ... (1229)

<223> UGT1A7*1

<400> 60

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<210> 61
 <211> 1229
 <212> DNA
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<220>
 <221> allele
 <222> (1)...(1229)
 <223> UGT1A7*2

<400> 61						
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 <223> UGT1A7*3

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<210> 63

<211> 1229

<212> DNA

<213> Homo sapiens

<220>

<221> allele

<222> (1)...(1229)

<223> UGT1A7*4

<400> 63

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<210> 64

<211> 1229

<212> DNA

<213> Homo sapiens

<220>

<221> allele

<222> (1)...(1229)

<223> UGT1A7*5

<400> 64

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<210> 65

<211> 1229

<212> DNA

<213> Homo sapiens

<220>

<221> allele

<222> (1) ... (1229)

<223> UGT1A7*6

<400> 65

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aggctgcaat	ctaaatgcta	tttttgga	aatacaaaaa	aaccacagta	agaaatgaaa	1140
cttccctttt	tttgctaatt	ctacactacc	cccagaggaa	aatattctta	gcagttttgt	1200
gtgaattggt	ttcaattttt	ttgaaatta				1229

<210> 66

<211> 1229
 <212> DNA
 <213> Homo sapiens

<220>
 <221> allele
 <222> (1)...(1229)
 <223> UGT1A7*7

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 atgcagtcgg tgggtggagaa actcatcctc agggggcatg aggtggtcgt agtcatgcca 180
 gaggtgagtt ggcaactggg aagatcactg aattgcacag tgaagactta ctcaacctca 240
 tacactctgg aggatcagga ccgggagttc atgggtttttg ccgatgctcg ctggacggca 300
 ccattgcgaa gtgcattttc tctattaaca agttcatcca atgggtatatt tgacttatatt 360
 ttttcaaatt gcaggagttt gtttaaggac aaaaaattag tagaatactt aaaggacagt 420
 tgttttgatg cagtgtttct cgatcctttt gatgcctgtg gcttaattgt tgccaaatat 480
 ttctccctcc cctctgtggg cttcgccagg ggaatatatt gccactatct tgaagaaggt 540
 gcacagtgcc ctgctcctct ttcctatgtc ccagacttc tcttaggggt ctcagacgcc 600
 atgactttca aggagagagt atggaaccac atcatgcact tggaggaaca tttattttgc 660
 ccctattttt tcaaaaatgt cttagaaata gcctctgaaa ttctccaaac ccctgtcacg 720
 gcatatgac tctacagcca cacatcaatt tgggtgttgc gaactgactt tgttttggag 780
 tatcccaaac ccgtgatgcc caatatgac ttcattgggt gtatcaactg tcatcaggga 840
 aagccagtgc ctatggttaag ttatctcccc ttttagcacat taagaataat ctggcctttgg 900
 aaattaaaag atttcttaca gaatcataat ttatcattta catttgtccc atttgaatt 960
 tctttctggg ttaaggaatt cttttgtacc aattcactta attgttgggt agcaaattgt 1020
 ataaagcagc tcttgttgat atgtaagtgt atacaattga tataattgta gatcatatct 1080
 aggctgcaat ctaaattgcta tttttggaaa aatacaaaaa aaccacagta agaaatgaaa 1140
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 gtgaattgtt ttcaattttt ttgaaatta 1229

<210> 67
 <211> 1229
 <212> DNA
 <213> Homo sapiens

<220>
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 <223> UGT1A7*8

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 atgcagtcgg tgggtggagaa actcatcctc agggggcatg aggtggtcgt agtcatgcca 180
 gaggtgagtt ggcaactggg aagatcactg aattgcacag tgaagactta ctcaacctca 240
 tacactctgg aggatcagga ccgggagttc atgggtttttg ccgatgctcg ctggacggca 300
 ccattgcgaa gtgcattttc tctattaaca agttcatcca atgggtatatt tgacttatatt 360
 ttttcaaatt gcaggagttt gtttaaggac aaaaaattag tagaatactt aaaggacagt 420
 tgttttgatg cagtgtttct cgatcctttt gatgcctgtg gcttaattgt tgccaaatat 480
 ttctccctcc cctctgtggg cttcgccagg ggaatatatt gccactatct tgaagaaggt 540
 gcacagtgcc ctgctcctct ttcctatgtc ccagacttc tcttaggggt ctcagacgcc 600
 atgactttca aggagagagt acggaaccac atcatgcact tggaggaaca tttattttgc 660
 ccctattttt tcaaaaatgt cttagaaata gcctctgaaa ttctccaaac ccctgtcacg 720
 gcatatgac tctacagcca cacatcaatt tgggtgttgc gaactgactt tgttttggag 780
 tatcccaaac ccgtgatgcc caatatgac ttcattgggt gtatcaactg tcatcaggga 840

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aaattaaaag	atttcttaca	gaatcataat	ttatcattta	catttgtccc	atttggaatt	960
tctttctggg	ttaaggaatt	cttttgtacc	aattcactta	attggtgggt	agcaaattgt	1020
ataaagcagc	tcttggtgat	atgtaagtgt	atacaattga	tataattgta	gatcatatct	1080
aggctgcaat	ctaaatgcta	tttttggaaa	aatacaaaaa	aaccacagta	agaaatgaaa	1140
cttccctttt	tttgctaatt	ctacactacc	cccagaggaa	aatattctta	gcagttttgt	1200
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<210> 68

<211> 1229

<212> DNA

<213> Homo sapiens

<220>

<221> allele

<222> (1) ... (1229)

<223> UGT1A7*9

<400> 68

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atgcagtcgg	tgggtggagaa	actcatcctc	agggggcatg	agggtggcgt	agtcatgcca	180
gaggtgagtt	ggcaactggg	aagatcactg	aattgcacag	tgaagactta	ctcaacctca	240
tacactctgg	aggatcagga	ccgggagttc	atgggtttttg	ccgatgctcg	ctggacggca	300
ccattgcgaa	gtgcattttc	tctattaaca	agttcatcca	atagtatttt	tgacttattt	360
ttttcaaatt	gcaggagttt	gtttaaggac	aaaaaattag	tagaatactt	aaaggagagt	420
tgttttgatg	cagtgtttct	cgatcctttt	gatgcctgtg	gcttaattgt	tgccaaatat	480
ttctccctcc	cctctgtggg	cttcgccagg	ggaatatttt	gccactatct	tgaagaaggt	540
gcacagtggc	ctgtcctctt	ttcctatgtc	cccagacttc	tcttaggggt	ctcagacgcc	600
atgactttca	aggagagagt	atggaaccac	atcatgcaact	tggaggaaca	tttattttgc	660
ccctattttt	tcaaaaatgt	cttagaaata	gcctctgaaa	ttctccaaac	ccctgtcacg	720
gcatatgatc	tctacagcca	cacatcaatt	tgggtgttgc	gaactgactt	tgttttggag	780
tatcccaaac	ccgtgatgcc	caatatgatc	ttcattgggtg	gtatcaactg	tcacagggga	840
aagccagtgc	ctatggtaag	ttatctcccc	tttagcacat	taagaataat	ctggccttgg	900
aaattaaaag	atttcttaca	gaatcataat	ttatcattta	catttgtccc	atttggaatt	960
tctttctggg	ttaaggaatt	cttttgtacc	aattcactta	attggtgggt	agcaaattgt	1020
ataaagcagc	tcttggtgat	atgtaagtgt	atacaattga	tataattgta	gatcatatct	1080
aggctgcaat	ctaaatgcta	tttttggaaa	aatacaaaaa	aaccacagta	agaaatgaaa	1140
cttccctttt	tttgctaatt	ctacactacc	cccagaggaa	aatattctta	gcagttttgt	1200
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<210> 69

<211> 530

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1) ... (530)

<223> UGT1A9*1 protein

<400> 69

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			20					25					30		
Met	Asp	Gly	Ser	His	Trp	Phe	Thr	Met	Arg	Ser	Val	Val	Glu	Lys	Leu

		35					40					45				
Ile	Leu	Arg	Gly	His	Glu	Val	Val	Val	Val	Met	Pro	Glu	Val	Ser	Trp	
	50					55					60					
Gln	Leu	Gly	Arg	Ser	Leu	Asn	Cys	Thr	Val	Lys	Thr	Tyr	Ser	Thr	Ser	
65					70					75					80	
Tyr	Thr	Leu	Glu	Asp	Leu	Asp	Arg	Glu	Phe	Lys	Ala	Phe	Ala	His	Ala	
				85					90					95		
Gln	Trp	Lys	Ala	Gln	Val	Arg	Ser	Ile	Tyr	Ser	Leu	Leu	Met	Gly	Ser	
			100					105					110			
Tyr	Asn	Asp	Ile	Phe	Asp	Leu	Phe	Phe	Ser	Asn	Cys	Arg	Ser	Leu	Phe	
		115					120				125					
Lys	Asp	Lys	Lys	Leu	Val	Glu	Tyr	Leu	Lys	Glu	Ser	Ser	Phe	Asp	Ala	
	130					135					140					
Val	Phe	Leu	Asp	Pro	Phe	Asp	Asn	Cys	Gly	Leu	Ile	Val	Ala	Lys	Tyr	
145					150					155					160	
Phe	Ser	Leu	Pro	Ser	Val	Val	Phe	Ala	Arg	Gly	Ile	Leu	Cys	His	Tyr	
				165					170					175		
Leu	Glu	Glu	Gly	Ala	Gln	Cys	Pro	Ala	Pro	Leu	Ser	Tyr	Val	Pro	Arg	
			180					185					190			
Ile	Leu	Leu	Gly	Phe	Ser	Asp	Ala	Met	Thr	Phe	Lys	Glu	Arg	Val	Arg	
		195					200					205				
Asn	His	Ile	Met	His	Leu	Glu	Glu	His	Leu	Leu	Cys	His	Arg	Phe	Phe	
	210					215					220					
Lys	Asn	Ala	Leu	Glu	Ile	Ala	Ser	Glu	Ile	Leu	Gln	Thr	Pro	Val	Thr	
225					230					235					240	
Glu	Tyr	Asp	Leu	Tyr	Ser	His	Thr	Ser	Ile	Trp	Leu	Leu	Arg	Thr	Asp	
				245					250					255		
Phe	Val	Leu	Asp	Tyr	Pro	Lys	Pro	Val	Met	Pro	Asn	Met	Ile	Phe	Ile	
			260					265					270			
Gly	Gly	Ile	Asn	Cys	His	Gln	Gly	Lys	Pro	Leu	Pro	Met	Glu	Phe	Glu	
		275					280					285				
Ala	Tyr	Ile	Asn	Ala	Ser	Gly	Glu	His	Gly	Ile	Val	Val	Phe	Ser	Leu	
	290					295					300					
Gly	Ser	Met	Val	Ser	Glu	Ile	Pro	Glu	Lys	Lys	Ala	Met	Ala	Ile	Ala	
305					310					315					320	
Asp	Ala	Leu	Gly	Lys	Ile	Pro	Gln	Thr	Val	Leu	Trp	Arg	Tyr	Thr	Gly	
				325					330					335		
Thr	Arg	Pro	Ser	Asn	Leu	Ala	Asn	Asn	Thr	Ile	Leu	Val	Lys	Trp	Leu	
			340					345					350			
Pro	Gln	Asn	Asp	Leu	Leu	Gly	His	Pro	Met	Thr	Arg	Ala	Phe	Ile	Thr	
		355					360					365				
His	Ala	Gly	Ser	His	Gly	Val	Tyr	Glu	Ser	Ile	Cys	Asn	Gly	Val	Pro	
	370					375					380					
Met	Val	Met	Met	Pro	Leu	Phe	Gly	Asp	Gln	Met	Asp	Asn	Ala	Lys	Arg	
385					390					395						

Leu Thr Val Ala Phe Ile Thr Phe Lys Cys Cys Ala Tyr Gly Tyr Arg
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 Lys Cys Leu Gly Lys Lys Gly Arg Val Lys Lys Ala His Lys Ser Lys
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 Thr His
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<210> 70
 <211> 530
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)...(50)
 <223> UGT1A9*2 protein

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 20 25 30
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 35 40 45
 Ile Leu Arg Gly His Glu Val Val Val Met Pro Glu Val Ser Trp
 50 55 60
 Gln Leu Gly Arg Ser Leu Asn Cys Thr Val Lys Thr Tyr Ser Thr Ser
 65 70 75 80
 Tyr Thr Leu Glu Asp Leu Asp Arg Glu Phe Lys Ala Phe Ala His Ala
 85 90 95
 Gln Trp Lys Ala Gln Val Arg Ser Ile Tyr Ser Leu Leu Met Gly Ser
 100 105 110
 Tyr Asn Asp Ile Phe Asp Leu Phe Phe Ser Asn Cys Arg Ser Leu Phe
 115 120 125
 Lys Asp Lys Lys Leu Val Glu Tyr Leu Lys Glu Ser Ser Phe Asp Ala
 130 135 140
 Val Phe Leu Asp Pro Phe Asp Asn Cys Gly Leu Ile Val Ala Lys Tyr
 145 150 155 160
 Phe Ser Leu Pro Ser Val Val Phe Ala Arg Gly Ile Leu Cys His Tyr
 165 170 175
 Leu Glu Glu Gly Ala Gln Cys Pro Ala Pro Leu Ser Tyr Val Pro Arg
 180 185 190
 Ile Leu Leu Gly Phe Ser Asp Ala Met Thr Phe Lys Glu Arg Val Arg
 195 200 205
 Asn His Ile Met His Leu Glu Glu His Leu Leu Cys His Arg Phe Phe
 210 215 220
 Lys Asn Ala Leu Glu Ile Ala Ser Glu Ile Leu Gln Thr Pro Val Thr
 225 230 235 240
 Glu Tyr Asp Leu Tyr Ser His Thr Ser Ile Trp Leu Leu Arg Thr Asp
 245 250 255
 Phe Val Leu Asp Tyr Pro Lys Pro Val Met Pro Asn Met Ile Phe Ile
 260 265 270
 Gly Gly Ile Asn Cys His Gln Gly Lys Pro Leu Pro Met Glu Phe Glu
 275 280 285
 Ala Tyr Ile Asn Ala Ser Gly Glu His Gly Ile Val Val Phe Ser Leu
 290 295 300
 Gly Ser Met Val Ser Glu Ile Pro Glu Lys Lys Ala Met Ala Ile Ala

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305          310          315          320
Asp Ala Leu Gly Lys Ile Pro Gln Thr Val Leu Trp Arg Tyr Thr Gly
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Thr Arg Pro Ser Asn Leu Ala Asn Asn Thr Ile Leu Val Lys Trp Leu
          340          345          350
Pro Gln Asn Asp Leu Leu Gly His Pro Met Thr Arg Ala Phe Ile Thr
          355          360          365
His Ala Gly Ser His Gly Val Tyr Glu Ser Ile Cys Asn Gly Val Pro
          370          375          380
Met Val Met Met Pro Leu Phe Gly Asp Gln Met Asp Asn Ala Lys Arg
385          390          395          400
Met Glu Thr Lys Gly Ala Gly Val Thr Leu Asn Val Leu Glu Met Thr
          405          410          415
Ser Glu Asp Leu Glu Asn Ala Leu Lys Ala Val Ile Asn Asp Lys Ser
          420          425          430
Tyr Lys Glu Asn Ile Met Arg Leu Ser Ser Leu His Lys Asp Arg Pro
          435          440          445
Val Glu Pro Leu Asp Leu Ala Val Phe Trp Val Glu Phe Val Met Arg
          450          455          460
His Lys Gly Ala Pro His Leu Arg Pro Ala Ala His Asp Leu Thr Trp
465          470          475          480
Tyr Gln Tyr His Ser Leu Asp Val Ile Gly Phe Leu Leu Ala Val Val
          485          490          495
Leu Thr Val Ala Phe Ile Thr Phe Lys Cys Cys Ala Tyr Gly Tyr Arg
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Lys Cys Leu Gly Lys Lys Gly Arg Val Lys Lys Ala His Lys Ser Lys
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Thr His
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<210> 71

<211> 530

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(530)

<223> UGT1A9*3 protein

<400> 71

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Thr Asp Gly Ser His Trp Phe Thr Met Arg Ser Val Val Glu Lys Leu
          35          40          45
Ile Leu Arg Gly His Glu Val Val Val Met Pro Glu Val Ser Trp
          50          55          60
Gln Leu Gly Arg Ser Leu Asn Cys Thr Val Lys Thr Tyr Ser Thr Ser
65          70          75          80
Tyr Thr Leu Glu Asp Leu Asp Arg Glu Phe Lys Ala Phe Ala His Ala
          85          90          95
Gln Trp Lys Ala Gln Val Arg Ser Ile Tyr Ser Leu Leu Met Gly Ser
          100          105          110
Tyr Asn Asp Ile Phe Asp Leu Phe Phe Ser Asn Cys Arg Ser Leu Phe
          115          120          125

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Lys Asp Lys Lys Leu Val Glu Tyr Leu Lys Glu Ser Ser Phe Asp Ala
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 Val Phe Leu Asp Pro Phe Asp Asn Cys Gly Leu Ile Val Ala Lys Tyr
 145 150 155 160
 Phe Ser Leu Pro Ser Val Val Phe Ala Arg Gly Ile Leu Cys His Tyr
 165 170 175
 Leu Glu Glu Gly Ala Gln Cys Pro Ala Pro Leu Ser Tyr Val Pro Arg
 180 185 190
 Ile Leu Leu Gly Phe Ser Asp Ala Met Thr Phe Lys Glu Arg Val Arg
 195 200 205
 Asn His Ile Met His Leu Glu His Leu Leu Cys His Arg Phe Phe
 210 215 220
 Lys Asn Ala Leu Glu Ile Ala Ser Glu Ile Leu Gln Thr Pro Val Thr
 225 230 235 240
 Glu Tyr Asp Leu Tyr Ser His Thr Ser Ile Trp Leu Leu Arg Thr Asp
 245 250 255
 Phe Val Leu Asp Tyr Pro Lys Pro Val Met Pro Asn Met Ile Phe Ile
 260 265 270
 Gly Gly Ile Asn Cys His Gln Gly Lys Pro Leu Pro Met Glu Phe Glu
 275 280 285
 Ala Tyr Ile Asn Ala Ser Gly Glu His Gly Ile Val Val Phe Ser Leu
 290 295 300
 Gly Ser Met Val Ser Glu Ile Pro Glu Lys Lys Ala Met Ala Ile Ala
 305 310 315 320
 Asp Ala Leu Gly Lys Ile Pro Gln Thr Val Leu Trp Arg Tyr Thr Gly
 325 330 335
 Thr Arg Pro Ser Asn Leu Ala Asn Asn Thr Ile Leu Val Lys Trp Leu
 340 345 350
 Pro Gln Asn Asp Leu Leu Gly His Pro Met Thr Arg Ala Phe Ile Thr
 355 360 365
 His Ala Gly Ser His Gly Val Tyr Glu Ser Ile Cys Asn Gly Val Pro
 370 375 380
 Met Val Met Met Pro Leu Phe Gly Asp Gln Met Asp Asn Ala Lys Arg
 385 390 395 400
 Met Glu Thr Lys Gly Ala Gly Val Thr Leu Asn Val Leu Glu Met Thr
 405 410 415
 Ser Glu Asp Leu Glu Asn Ala Leu Lys Ala Val Ile Asn Asp Lys Ser
 420 425 430
 Tyr Lys Glu Asn Ile Met Arg Leu Ser Ser Leu His Lys Asp Arg Pro
 435 440 445
 Val Glu Pro Leu Asp Leu Ala Val Phe Trp Val Glu Phe Val Met Arg
 450 455 460
 His Lys Gly Ala Pro His Leu Arg Pro Ala Ala His Asp Leu Thr Trp
 465 470 475 480
 Tyr Gln Tyr His Ser Leu Asp Val Ile Gly Phe Leu Leu Ala Val Val
 485 490 495
 Leu Thr Val Ala Phe Ile Thr Phe Lys Cys Cys Ala Tyr Gly Tyr Arg
 500 505 510
 Lys Cys Leu Gly Lys Lys Gly Arg Val Lys Lys Ala His Lys Ser Lys
 515 520 525
 Thr His
 530